

Fig. 1

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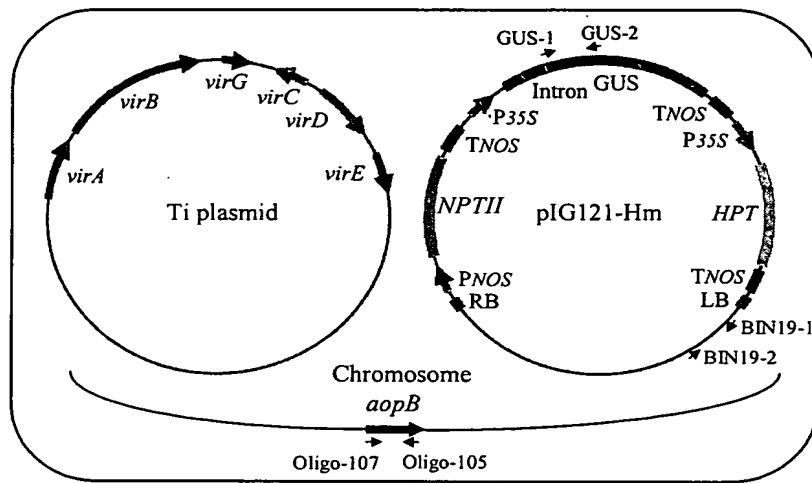


Fig. 2

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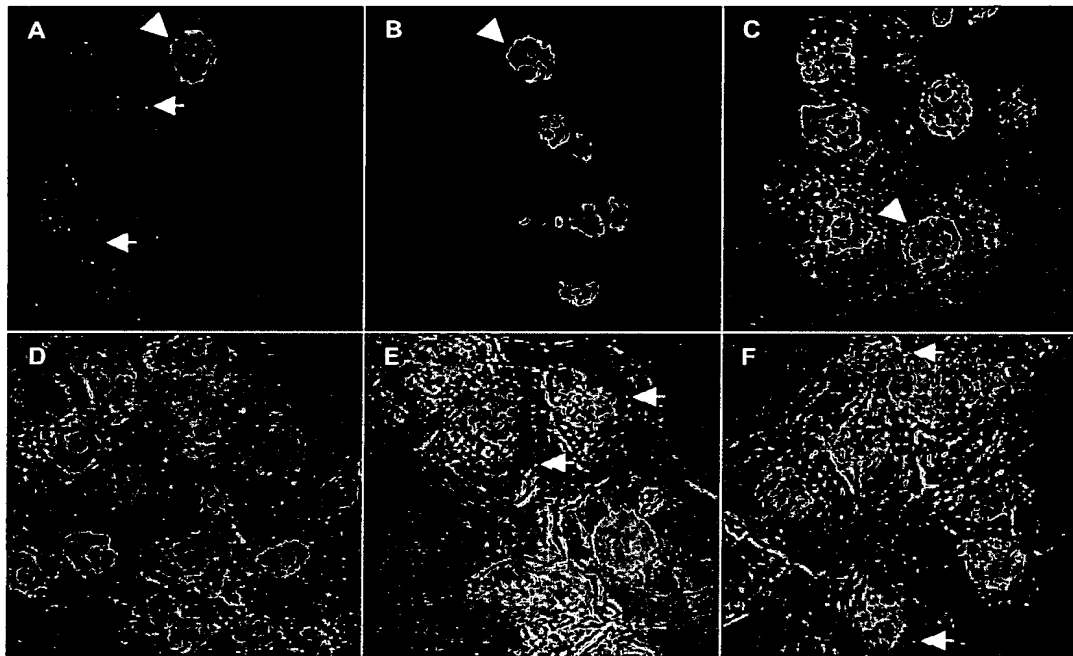


Fig. 3

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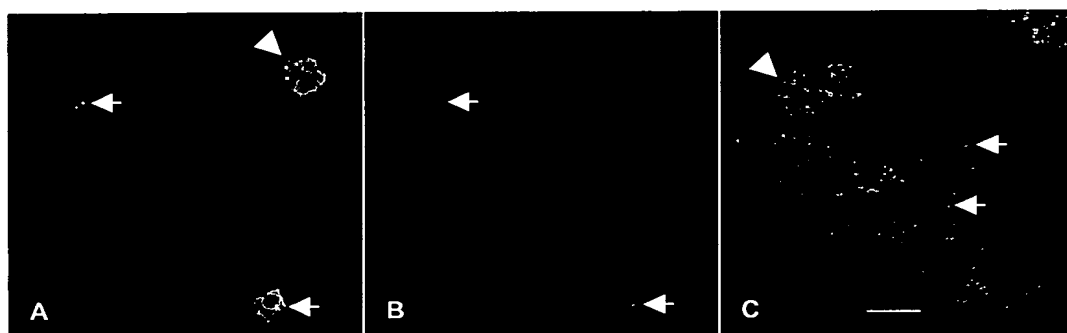


Fig. 4

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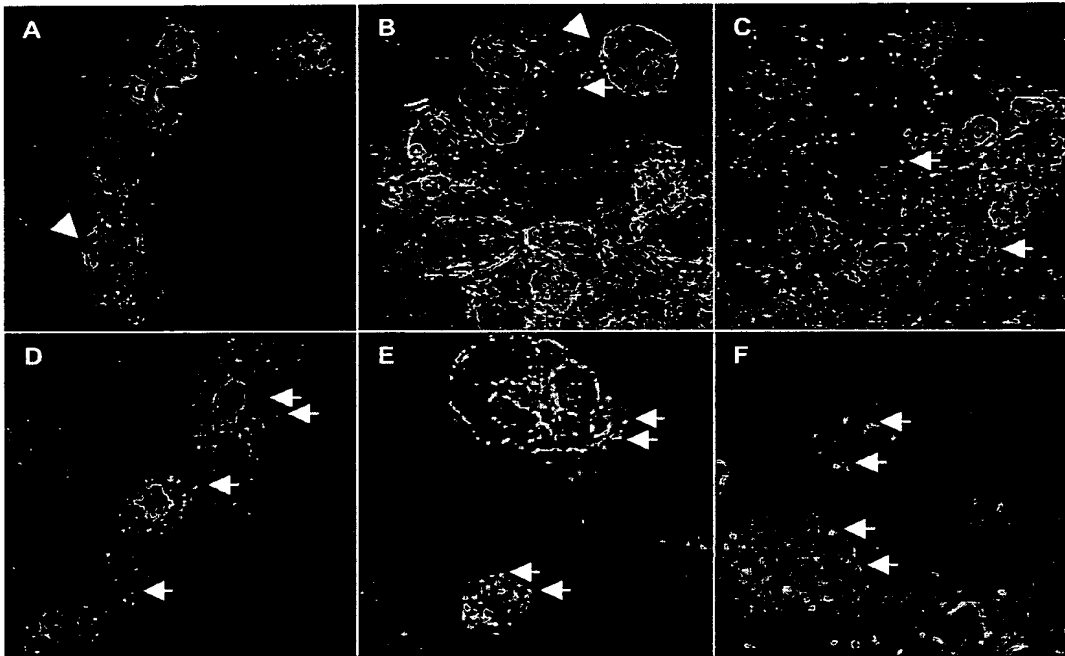


Fig. 5

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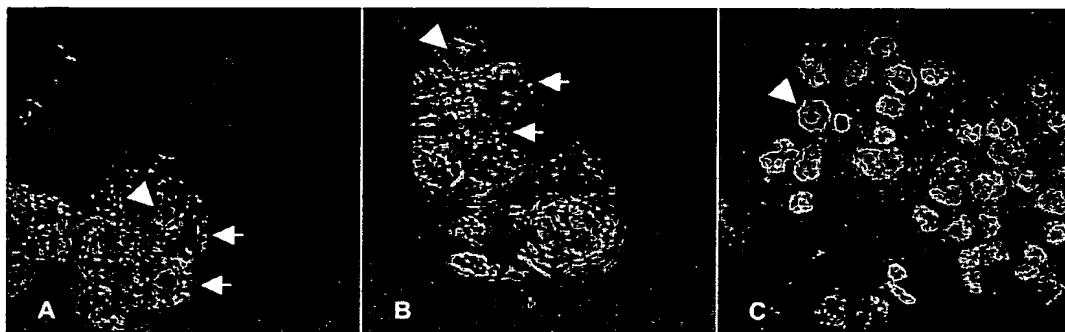


Fig. 6

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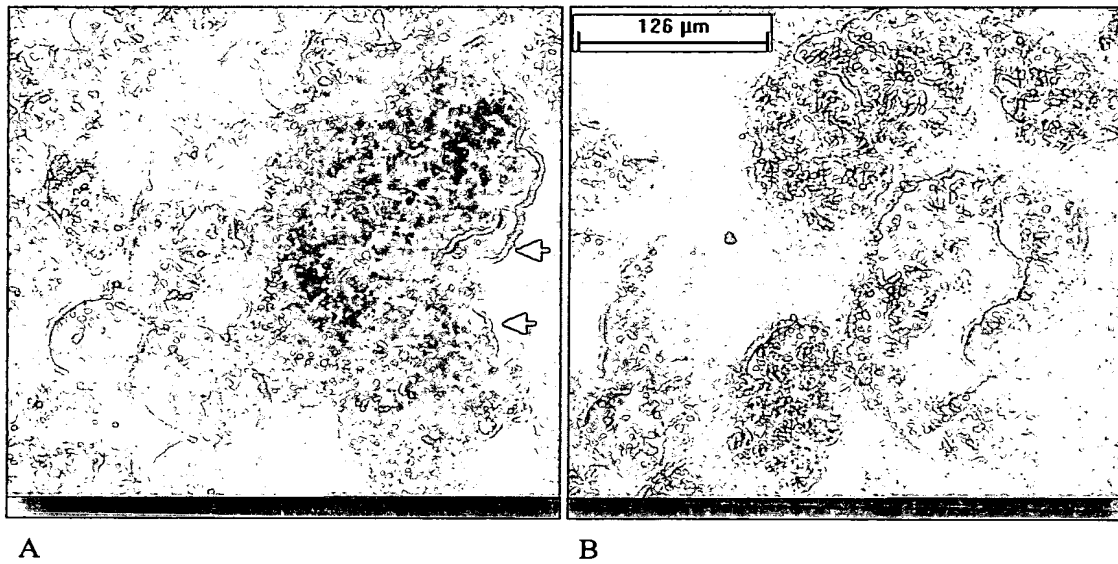


Fig. 7

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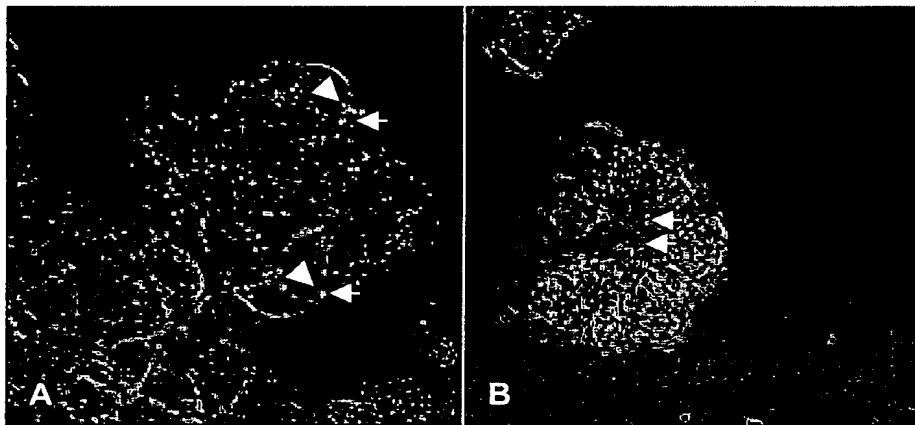


Fig. 8

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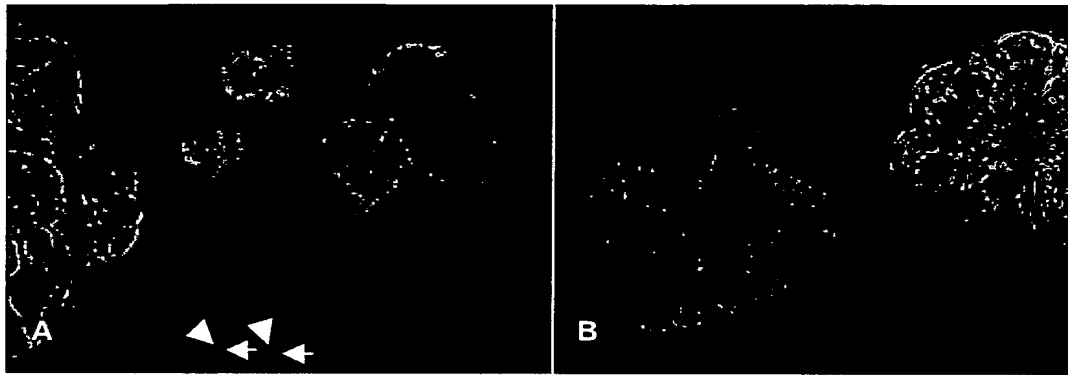




FIG. 9: VDI sequence (top) vs Sec3 Homologs (bottom)

Q9NV70 Human Exocyst complex component Sec3 (BM-012)		Length = 894
5	Query: 55 LALS VKSKGPRKKAFLRVMKYSSGGVLEPAKMYKLKHL SKVEVITNDPSGCTFTLGFDNL 114	
	L +V ++ P + ++V K G + + L+ L+ V+ F L F+ +	
	Sbjct: 38 LCATVTTERPVQVKVVKVKS DKGDFYKRQIAWALRDLAVDAKDAIKENPEFDLHFEKI 97	
10	Query: 115 RSQS VAPPQWTRNTDDRNRLLVCILNICKDVLGR LPKVVGIDIVEMALWAKDNTPVVTT 174	
	+W +T ++N + CI + + L + ID V N	
	Sbjct: 98 Y-----KWVASSTA EKNAFISCIWKL NQRYLRK-----KIDFV-----NVSSQLL 137	
	Query: 175 QRSTEDGEPVAESVTESDLKVTVEKELVSQAEEEDMEALLGTYVMGIGEEAFSERLKRE 234	
	+ S GE +SVT D +V E + ++ EE+D+E ++ I AEAF+E+L RE	
15	Sbjct: 138 EESVPSGE--NQSVTGGDEEVVDEYQELNAREEQDIEIMMEGCEY AISNAEAFAEKLSRE 195	
	Query: 235 LQALEAANVHAILESEPLVDEV LNGLEAATNIVDDMDEWL GIFNIKL RHREDIESIETR 294	
	LQ L+ AN+ +I+ SE V+ ++ L+ A VD ++ L + L+ ++E ++ I	
20	Sbjct: 196 LQVLDGANIQSIMASEKQVNILMKLLDEALKEVDQIELKLSSYEEM LQSVKEQMDQISES 255	
	Query: 295 NNKLEMQSVNNKALIEELD KVIERLRVPSEYAASLTGGSFDEADMLQNI EACEWLAKALR 354	
	N+ + + + NN L+ E++ ++ + + + +L G + + IEAC A AL	
	Sbjct: 256 NHLIHL SNTNNV KLLSEIEFLVNHMDLAKGH IKALQEGDLASS---RGIEACTNAADALL 312	
25	Query: 355 GLEVPNLDPIYANMR AVKEKRAELEKLKATFVRRASEFLRNYFASLVDFM VSDKSYFSQR 414	
	L P + + AVK ++ L+ F RR + L N F V S +Q	
	Sbjct: 313 QCMNVALRPGHDL LLA VKQQQRFSDLR ELFARRLASHLNNVF---VQQGHDQSSTLAQH 369	
30	Query: 415 G-QLKRPDHADLR YKCR TYARLLQHLKGLDKNCLG PLRKAYCSSLNLLLRREAREFAN-- 471	
	+L P+H YA+L++ LK D L K Y L+ L RE ++F	
	Sbjct: 370 SVELTLPNHHPFHRDLLRYAKLMEWL KSTDYGYEGLTKNYMDYLSRLYEREIKDFFEVA 429	
	Query: 472 --ELRASTKVS-----RNPTVWLEGSTG-----SSQNANTDT 501	
	++ +TK S + T L GS+G SS N + +	
35	Sbjct: 430 KIKMTGTTKESKKFATLPRKESAVKQETESLHGSSGKLTGSTSSLNKL SVQSSGNRRSQS 489	
	Query: 502 SAVSDA-----YAKMLTIFIPLLVDESSFFAHFMC FEVPALAPPGG 542	
	S++ D + ++L+ PL + E F + F + + PG	
40	Sbjct: 490 SSLDMDGNMSASDL DVADRTKFDKIFEQVLSELEPLCLAEQDFISKFFKLQ-QHQSM PG 548	
	Query: 543 AGNDKKSQSNDDGND DDDLGIMDIDETDKKPGKNSPDLTALNESLQD LLDGIQEDFYAV 602	
	E D + + + + I+ + +	
	Sbjct: 549 MAEAEDLDGGT LSRQHNCGTPLPVSSEKD-----MIRQMMIKIFRCIEPELNNL 597	
45	Query: 603 VDWAYKIDPLRCISM H-GITER YLSGQKADAAGFVRLL LGDLESRVSMQFSRFVDEACHQ 661	
	+ KID + M ++ + Q D A F+ LG++ V F + + Q	
	Sbjct: 598 IALGDKIDSFN SLYMLVKMSHHVWTAQNVD PASFLSTLGNVLVTVKRNF DKCISNQIRQ 657	
	Query: 662 IERNERNVR-QMGVLPYIPRFAALATRMEQ-YIQGQSRDLVDQAYTKFVSIMFVTLEKIA 719	
	+E + + + ++G+LP++ F A E + + R +D+AYTK + +FV +EK+A	
50	Sbjct: 658 MEEVKISKKSKVGILPFVAEFEEFAGLAESIFKNAERRGDL DKAYTKLIRGVFVNVEKVA 717	
	Query: 720 QQDPKYA-DILLLENYA AFQNSLYDLANVVPTLAKFYHQASEAYEQACTRHISMIIYYQF 778	
	+ K D++++EN+ +L L + L +A + Y ++ +	
55	Sbjct: 718 NESQKTPRDVMMENFHHIFATLSRLK--ISCLEAEKKEAKQKYTDHLQSYVIYSLGQPL 775	

## FIG. 9 Cont'd

- Query: 779 ERLFQFAKKIEDFMYT-ITPEEIPFQLGLSKVELRKMLKSSLSG-VDKSIAAMYKKLQKN 836  
 E+L F + +E + I EE+ +QL +K ELRK++K V K + +YKK+ K+  
 5 Sbjct: 776 EKLNHFFEGVEARVAQGIREEEVSQYLA FNKQELRKVIKEYPGKEVKKGLDNLYKKVKDKH 835
- Query: 837 LASEE-LLPSLWDKCKKEFLDKYESFVQLVAKVYPSENV 874  
 L EE LL +W + EF+ +Y+ F L+A+ YP V  
 10 Sbjct: 836 LCEEENLLQVVWHSMQDEFIRQYKHFEGLIARCYPGSGV 874
- XP 223340.1 similar to Exocyst complex component Sec3 [*Rattus norvegicus*]  
 Length = 571
- 15 Query: 626 SGQKADAAGFVRLLLGDLESRVSMQFSRFVDEACHQIERNERNVR-QMGVLPYIPRFAAL 684  
 + Q D A F+ LG++ V F + + Q+E + + + ++G+LP++ F  
 Sbjct: 299 TAQNVDPASFLSTTLGNVLVTVKRNFDKCISNQIRQMEEVKISKSKVGILPFVAEFEEF 358
- 20 Query: 685 ATRMEQ-YIQGQSRDLVDQAYTKFVSIMFVTLEKIAQQDPKYA-DILLLENYA AFQNSLY 742  
 A E + + R +D+AYTK + +F+ +EK+A + K D++++EN+ +L  
 Sbjct: 359 AGLAESIFKSAERRGDLDAKAYTKLRGVFINVEKVANESQKTPRDRVMMENFHHIFATLS 418
- Query: 743 DLANVVPTLAKFYHQASEAYEQACTRHISMIIYYQFERLQFAKKIEDFMYT-ITPEEIP 801  
 L + L +A + Y ++ + E+L F + +E + I EE+  
 25 Sbjct: 419 RLK--ISCLEAEKKEAKQKYTDHLQSYVIYSLGQPLEKLNHFFEGVEARVAQGIREEEVS 476
- Query: 802 FQLGLSKVELRKMLKSSLSG-VDKSIAAMYKKLQKNLASEE-LLPSLWDKCKKEFLDKYE 859  
 +QL +K ELRK++K V K + +YKK+ K+L EE LL +W + EF+ +Y+  
 30 Sbjct: 477 YQLAFNKQELRKVIKEYPGKEVKKGLDNLYKKVKDKHLCEEENLLQVVWHSMQDEFIRQYK 536
- Query: 860 SFVQLVAKVYPSENV 874  
 F L+A+ YP V  
 Sbjct: 537 HFEGLIARCYPGSGV 551
- 35 Q8R3S6 SEC3 Mouse Exocyst complex component Sec3  
 AAH24678.1| Similar to Sec3-like [*Mus musculus*] Length = 894
- 40 Query: 55 LALSVKSKGPRKKAFLRVMKYSSGGVLEPAKMYKLKHLKSKVEVITNDPSGCTFTLGFNDL 114  
 L +V ++ P + ++V K G + + L+ L+ V+ F L F+ +  
 Sbjct: 38 LCATVTTERPVQVKVVKVKKSDKGDFYKQIAWALRDLAVVDAKDAIKENPEFDLHFEKV 97
- Query: 115 RSQSVAPPQWMTMRNTDDRNRLVCILNICKDVLGRLPKVVGIDIVEMALWAKDNTPVVTT 174  
 +W +T ++N + CI + + L + ID V N  
 45 Sbjct: 98 Y-----KWVASSTAENAFISCIWKLNRQYLRK-----KIDFV-----NVSSQLL 137
- Query: 175 QRSTEDGEPPVAESVTESDLKVTVEKELVSQAEEDMEALLGTYVMGIGEAFAFSERLKRE 234  
 + S GE +SV D + E + ++ EE+D+E ++ I AEAF+E+L RE  
 50 Sbjct: 138 EESVPSGE--NQSVAGGDEEAVDEYQELNAREEQDIEIMMEGCECAISNAEFAEKL SRE 195
- Query: 235 LQALEAANVHAILESEPLVDEVLNGLEAATNIVDDMDEWL GIFNIKLRHMREDIESIETR 294  
 LQ L+ AN+ +I+ SE V+ ++ L+ A VD ++ L + L+ ++E ++ I  
 Sbjct: 196 LQVLDGANIQSIMASEKQVNTLMQLLDEALTEVDQIELKLSSYEMLQSVKEQMDQISES 255
- 55 Query: 295 NNKLEMQSVNNKALIEELDKVIERLRVPSEYAASLTGGSFDEADMLQNI EACEWLAKALR 354  
 N+ + + + NN L+ E++ ++ + + + +L G + + IEAC A AL  
 Sbjct: 256 NHLIHLSTNNVKLLSEIEFLVNHMDLAKGHKALQEGDLVSS---RGIEACTNAADALL 312

## FIG. 9 Cont'd

Query: 355 GLEVPNLDPIYANMRAVKEKRAELEKCLKATFVRRASEFLRNYFASLVDFMVSCKSYFSQR 414  
 L P + + A K ++ L+ F RR + L N F V S +Q

5 Sbjct: 313 QCMNVALRPGHDMMLAIKQQQQRFSDLREHFARRLASHLNNVF--VQQGHDQSSTLAQH 369  
 Query: 415 G-QLKRPDHADLRYKCRTYARLLQHLKGLDKNCLGPLRKAYCSSLNLLLRREAREF 469  
 +L P+H YA+L++ LK D L K Y L+ L RE ++F

Sbjct: 370 SVELTLPNHHFPHRDLLRYAKLMEWLKSTDYGYEGLTKNYMDYLSRLYEREIKDF 425

10 AAL29126.1 SD02883p [*Drosophila melanogaster*] Length = 889

Query: 123 QWTMRNTDDRNRLLVCILN--ICKDVLGRLPKVVGIDIVEMALWAKDNTTP-VVTTQRSTE 179  
 +W N +R L +LN I K V G+ + + A W + +P V R+ +

15 Sbjct: 105 KQYALNPHERQNFILA-VLNRIQKSVRGQRAEFRNVP---AAWLSEKSPKVALGRAVQ 159

Query: 180 DGEFVAESVTESDLKVTVEKELVSQAEEEDMEALLGTYVMGIGEAFAFSEKRLKRELQALE 239  
 + + E + + E ++ E ++ L I +AE F E+L REL L+

20 Sbjct: 160 KTQHM--DDEEDEEEEAQEFTALTDKEANELGKLFSECDFAIKDAEQFIEQLSRELHDL 217

Query: 240 AANVHAILESEPLVDEVINGLEAATNIVDDMDEWLGIKRLHMRDIESIETRNKLE 299  
 AN+ ++L SE V +++ ++ A + D + L + L H++E +E I +N +E

25 Sbjct: 218 GANMQSVLASEQKVLKMMEHIDNAISEADKFENRLDSYEDILGHVKETMEKIGGKNAMIE 277

Query: 300 MQSVNNKALIEELDKVIERLRVPSEYAAASLTGGSFDEADMLQ-NIEACEWLAKALRGLEV 358  
 + + NN L++EL+KVI +L +P +L A+ + I A + L +A+

Sbjct: 278 IANNNNIKLMKELNKVISQLDLPHSQQQALDEPDLTANGRKAIAAAQCLQQAMNS--- 334

30 Query: 359 PNLDPIYANMRAVKEKRAELEKCLKATFVRRASEFLRNYFASLVDFMVSCKSYFSQSGQLK 418  
 ++DP + AV++++ EK K F S F+ N F L + + D S +L

Sbjct: 335 -DIDPALLRLEAVQDQKRFEKWKQKFSATVSRFMNNLFIHLGN-EIGDMQVTST--ELT 390

Query: 419 RPDHADLRYKCRTYARLLQHLKGLDKNCLGPLRKAYCSSLNLLLRREAREFANELRAS-T 477  
 P+H+++ + Y L+ K +D+ L + Y +SL+ + R+ R F N + T

35 Sbjct: 391 LPNHSNVHRELTPYTELMHWTKAMDRKTYDGLMRVYTASLSKIYDRDVRNFFNLAKIQVT 450

Query: 478 KVS RNPTVWLEGSTGSSQNA-----NTDTSAVSDAYAKMLTIFI 516  
 + RN L+ ST S ++A D K+L

40 Sbjct: 451 EKLRNSREDLDMSTSSRKS AVSTIPYGTGLGINRDQWGPVETADRMRFDALLEKVLAELE 510

Query: 517 PLLVDESSFFAHFMCFEVPALAPPGGAGNDKKSQSNNDGNDDDLGMIDIDETDKKPGK 576  
 P+ + E F +F +V + P D P K

45 Sbjct: 511 PIALQEQLFCINFFQMDVIS---PTTKNTQTTEMEKAVDMTQSIISGAVSPSGDGVPOK 567

Query: 577 NSPDLTALNESLQDLLDG----IQEDFYAVVDWAYKIDPLRCISMH-GITERYLSGQKAD 631  
 +NE ++ L+ G ++ + + + ++D + + +T+ +S Q D

Sbjct: 568 RID--RQINEDVRKLMMGLFGCLEPELVSFQSFERVDSFYSLYVVRILTQHVMQAQ--D 623

50 Query: 632 AAGFVRLLLGDLES RVSMQFSRFVDEACHQIERNERNVRQMGVLPYIPRFAALATRMEQ- 690  
 F+ + +V F RF+ I + + R +LPY+ F A E

Sbjct: 624 THSFLSMTFASALVQVKRSFDRFMQNQLLSIREAKLHKRSKAILPYVENFENFAQTAEGI 683

Query: 691 YIQGQSRDLVDQAYTKFVSIMFVTLEKIAQQDPKYA-DILLLENYAAFQNSLYDLANVVP 749  
 + + R +++ Y + V+ +F ++ +Q+ PK ++ +ENY L L VP

55 Sbjct: 684 FRKSDRRTDMEKWYLQLVNAIFEGIQLHSQEHKPTPIQVVRMENYHHMYALLAQLK--VP 741

## FIG. 9 Cont'd

Query: 750 TLAKFYHQASEAYEQACTRHISMIIYYQFERLFQFAKKIE-DFMYTITPEEIPFQLGLSK 808  
L +A + Y A +++ E+L QF + ++ + EI +Q+ SK  
5 Sbjct: 742 GLDALKKEAKKCYNDALKAYVTQYFGRPLEKLNQFFEGVQLKVAQGVKETEISYQMAFSK 801

Query: 809 VELRKML-KSSLGVDKSIAMYKKLQKNLASEE-LLPSLWDKCKKEFLDKYESFVQLVA 866  
ELRK++ + V K + +YKK++K+L+ EE LL +W ++EF+ +Y + +  
10 Sbjct: 802 QELRKVIAQYPAREVKKGLENLYKKVEKHLSEEENLLQVVWHAMQEEFIAQYNYLEERIQ 861

Query: 867 K V Y 869  
K Y  
Sbjct: 862 K C Y 864

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